

SEQUENCE LISTING

<110> Glucksmann, Maria Alexandra
Silos-Santiago, Inmaculada

<120> Novel Seven-Transmembrane
Proteins/G-Protein Coupled Receptors

<130> 35800/208932

<150> 60/182,061

<151> 2000-02-11

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1875

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323)...(1522)

<221> misc_feature

<222> (1)...(1875)

<223> n = A,T,C or G

<400> 1

tcccccccct tttttttttt ttttttnnaa aggaagtccc acttggcccc ccaagnttga	60
agtcaagggc agatttgggn tcattgaacn tcacttccaa ggtcaaggat tctcatgctc	120
agtttgcaag gactgagatt acagtggcct gcacctggct tattttggta ttttaagtaa	180
agacaggggtt tcaccatggt ggccaggctg ttcttgaaact cctgacctca agtggtcccc	240
ntgcctcggg cctcccaaag tgctgggatt acaggcatga accaccatcc ccagccttct	300
ctctttttaa taatggcttt ct atg tct ttc act tct ctc ata ccc tca ctc	352
Met Ser Phe Thr Ser Leu Ile Pro Ser Leu	
1 5 10	

tgt ttc tcc ttg act ctc cca ttc ctg ttt tgt tat ctt tct tta tgg	400
Cys Phe Ser Leu Thr Leu Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp	
15 20 25	

ccg ttt ctt tct gct ttt ctg ttt atc act cgc tgg cta ctt gcc ttt	448
Pro Phe Leu Ser Ala Phe Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe	
30 35 40	

ctc tct cta ttc tct gtc tct gtc cct gtt tct tct gtt tca agt tca	496
Leu Ser Leu Phe Ser Val Ser Val Pro Val Ser Ser Val Ser Ser Ser	
45 50 55	

atg gtt ctc tgt ctc tat ctc tct gtt tct gcc tct ccg tct gtc ttt	544
---	-----

Abstract

agc cag ccc tcc gaa ttt gtc ctc ttg ggc ttc tcc tcc ttt ggt gag 640
 Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser Ser Phe Gly Glu
 95 100 105

ctg cag gcc ctt ctg tat ggc ccc ttc ctc atg ctt tat ctt ctc gcc 688
Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala
110 115 120

ttc atg gga aac acc atc atc ata gtt atg gtc ata gct gac acc cac 736
Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp Thr His
125 130 135

cta cat aca ccc atg tac ttc ttc ctg ggc aat ttt tcc ctg ctg gag 784
Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu
140 145 150

atc ttg gta acc atg act gca gtg ccc agg atg ctc tca gac ctg ttg 832
Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu
155 160 165 170

gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac 880
Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr
175 180 185

ttc cac ttt tcc ctg ggg tcc acc tcc ttc ctc atc ctg aca gac atg 928
Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met
190 195 200

gcc ctt gat cgc ttt gtg gcc atc tgc cac cca ctg cgc tat ggc act 976
Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr
205 210 215

ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct gcc tgg gca 1024
Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala
220 225 230

gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 1072
Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu
235 240 245 250

gat tac tgc cat ggc ggc gtc atc aac cac ttc ttc tgt gac aat gaa 1120
Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu
255 260 265

cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gaa ttc tgg 1168
Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp
270 275 280

gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ttc ctg gtg acc 1216
Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr
285 290 295

ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 1264
Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser
300 305 310

gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 1312
Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr
315 320 325 330

ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 1360
Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro
335 340 345

ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408
Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr
350 355 360

tca gtt ctc acc ccc ttt ctc aat ccc ttt atc ctt acc ttc tgc aat 1456
Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn
365 370 375

cag aca gtt aaa aca gtg cta cag ggg cag atg cag agg ctg aaa ggc 1504
Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln Arg Leu Lys Gly
380 385 390

ctt tgc aag gca caa tga tgagcccagg gccagggga acctggcctg 1552
Leu Cys Lys Ala Gln *
395

ctccattga	gcagttctgt	ggggagggag	acctccagca	agtgggaaga	acactgctga	1612
gtttcttttag	tttttttccc	tctgagcaat	aactacagtg	agccctgagt	gctgcaactgt	1672
ctggcccaaa	gctcttatgg	accaccatgg	aagagttccc	tacatcccct	ggcagccgta	1732
agaactctga	gagtagccca	gagctttcag	taaaggggaag	tgcattgtgct	ttgcatttaa	1792
ggaagagcag	cmagaagatg	ctctatgac	aagaggtagt	cgacgcggcc	gogtcgacgg	1852
aagctgggat	acagcattta	atg				1875

```
<210> 2
<211> 399
<212> PRT
<213> Homo sapiens
```

<400> 2															
Met	Ser	Phe	Thr	Ser	Leu	Ile	Pro	Ser	Leu	Cys	Phe	Ser	Leu	Thr	Leu
1				5					10					15	
Pro	Phe	Leu	Phe	Cys	Tyr	Leu	Ser	Leu	Trp	Pro	Phe	Leu	Ser	Ala	Phe
			20					25					30		
Leu	Phe	Ile	Thr	Arg	Trp	Leu	Leu	Ala	Phe	Leu	Ser	Leu	Phe	Ser	Val
		35				40						45			
Ser	Val	Pro	Val	Ser	Ser	Val	Ser	Ser	Ser	Met	Val	Leu	Cys	Leu	Tyr
	50					55					60				
Leu	Ser	Val	Ser	Ala	Ser	Pro	Ser	Val	Phe	Cys	Phe	Ser	Cys	Met	Gln
65					70					75					80

[illegible]

<400> 3							
atgtctttca	cttctctcat	accctcactc	tgtttctcct	tgactctccc	attcctgttt		60
tgttatcttt	ctttatggcc	gtttctttct	gcttttctgt	ttatcactcg	ctggctactt		120
gcctttctct	ctctattctc	tgtctctgtc	cctgtttctt	ctgtttcaag	ttcaatggtt		180
ctctgtctct	atctctctgt	ttctgcctct	ccgtctgtct	tttgtttctc	ttgcatgcag		240
ggccccatac	tgtggatcat	ggcaaatctg	agccagccct	ccgaatttgt	cctcttgggc		300
ttctcctctt	ttggtgagct	gcaggccctt	ctgtatggcc	ccttctctcat	gctttatctt		360
ctcgccttca	tgggaacac	catcatcata	gttatggtca	tagctgacac	ccacctacat		420
acacccatgt	actcttctct	qggcaatttt	tcctctgctq	aqatcttgqt	aaccatgact		480

gcagtgccca	ggatgctctc	agacctgttg	gtccccaca	aagtcattac	cttcactggc	540
tgcattggcc	agttctactt	ccacttttcc	ctgggggtcca	cctccttcc	catcctgaca	600
gacatggccc	ttgatcgctt	tgtggccatc	tgccaccac	tgcgctatgg	cactctgatg	660
agccgggcta	tgtgtgtcca	gctggctggg	gctgcctggg	cagctccttt	cctagccatg	720
gtacccactg	tcctctccc	agctcatctt	gattactgcc	atggcgcggt	catcaaccac	780
ttcttctgtg	acaatgaacc	tctcctgcag	ttgtcatgct	ctgacactcg	cctgttgga	840
ttctgggact	ttctgatggc	cttgaccttt	gtcctcagct	ccttccctgg	gacctcatc	900
tcctatggct	acatagtgc	cactgtgctg	cggtatccct	ctgccagcag	ctgccagaag	960
gctttctcca	cttgccgggtc	tcacctcaca	ctggtcttca	tcggctacag	tagtaccatc	1020
tttctgtatg	tcaggcctgg	caaagctcac	tctgtgcaag	tcaggaagg	cgtggccttg	1080
gtgacttcag	ttctacccc	ctttctcaat	ccctttatcc	ttaccttctg	caatcagaca	1140
gttaaaacag	tgctacagg	gcagatgcag	aggctgaaag	gcctttgcaa	ggcacaatga	1200

<210> 4
 <211> 3630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (343)...(2334)

<400> 4						
gcgtccggcc	gccgccggcg	cgcgccgcca	cgccggcgcc	ggctgctaag	gggctcggcc	60
cgcgagcgcc	tgctgccggc	gacgatggtg	accgtacggg	ccgggcccgt	gccgctgccg	120
ctgcctccgc	ctccccagaa	gcaacatccg	aggctcggcg	cagaagagcc	gccgctgtga	180
gccgtgccgt	accggccccc	gccgccgccc	gaggagaacg	ggaggcgggg	cgagagagcc	240
ggggagttgc	ggagcccgcc	cgccggcagc	gccgctcccc	agggaggag	tccgcagcct	300
gaggtcttct	ccaagaaaaa	aaaaaagaaa	aaaaaaaaaca	ac atg gct gca aag		354
					Met Ala Ala Lys	
					1	

gag	aaa	ctg	gag	gca	gtg	tta	aat	gtg	gcc	ctg	agg	gtg	cca	agc	atc	402
Glu	Lys	Leu	Glu	Ala	Val	Leu	Asn	Val	Ala	Leu	Arg	Val	Pro	Ser	Ile	
5					10					15					20	

atg	ctg	ttg	gat	gtc	ctg	tac	aga	tgg	gat	gtc	agc	tcc	ttt	ttc	cag	450
Met	Leu	Leu	Asp	Val	Leu	Tyr	Arg	Trp	Asp	Val	Ser	Ser	Phe	Phe	Gln	
			25						30					35		

cag	atc	caa	aga	agt	agc	ctt	agt	aat	aac	cct	ctt	ttc	cag	tat	aag	498
Gln	Ile	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu	Phe	Gln	Tyr	Lys	
			40					45					50			

tat	ttg	gct	ctt	aat	atg	cat	tat	gta	ggg	tat	atc	tta	agt	gtg	gtg	546
Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	Ile	Leu	Ser	Val	Val	
	55						60					65				

ctg	cta	aca	ttg	ccc	agg	cag	cat	ctg	gtt	cag	ctt	tat	cta	tat	ttt	594
Leu	Leu	Thr	Leu	Pro	Arg	Gln	His	Leu	Val	Gln	Leu	Tyr	Leu	Tyr	Phe	
	70					75				80						

ttg	act	gct	ctg	ctc	ctc	tat	gct	gga	cat	caa	att	tcc	agg	gac	tat	642
Leu	Thr	Ala	Leu	Leu	Leu	Tyr	Ala	Gly	His	Gln	Ile	Ser	Arg	Asp	Tyr	
	85					90				95					100	

gtt Val	cgg Arg	agt Ser	gaa Glu	ctg Leu 105	gag Glu	ttt Phe	gcc Ala	tat Tyr	gag Glu 110	gga Gly	cca Pro	atg Met	tat Tyr	tta Leu 115	gaa Glu	690
cct Pro	ctc Leu	tct Ser	atg Met 120	aat Asn	cgg Arg	ttt Phe	acc Thr 125	aca Thr	gcc Ala	tta Leu	ata Ile	ggg Gly	cag Gln 130	ttg Leu	gtg Val	738
gtg Val	tgt Cys	act Thr 135	tta Leu	tgc Cys	tcc Ser	tgt Cys	gtc Val 140	atg Met	aaa Lys	aca Thr	aag Lys	cag Gln 145	att Ile	tgg Trp	ctg Leu	786
ttt Phe 150	tca Ser	gct Ala	cac His	atg Met	ctt Leu	cct Pro	ctg Leu 155	cta Leu	gca Ala	cga Arg	ctc Leu 160	tgc Cys	ctt Leu	gtt Val	cct Pro	834
ttg Leu 165	gag Glu	aca Thr	att Ile	gtt Val 170	atc Ile	atc Ile	aat Asn	aaa Lys	ttt Phe	gct Ala 175	atg Met	att Ile	ttt Phe	act Thr 180	gga Gly	882
ttg Leu	gaa Glu	gtt Val	ctc Leu	tat Tyr 185	ttt Phe	ctt Leu	ggg Gly	tct Ser	aat Asn 190	ctt Leu	ttg Leu	gta Val	cct Pro	tat Tyr 195	aac Asn	930
ctt Leu	gct Ala	aaa Lys 200	tct Ser	gca Ala	tac Tyr	aga Arg	gaa Glu	ttg Leu 205	gtt Val	cag Gln	gta Val	gtg Val	gag Glu 210	gta Val	tat Tyr	978
ggc Gly	ctt Leu	ctc Leu 215	gcc Ala	ttg Leu	gga Gly	atg Met	tcc Ser 220	ctg Leu	tgg Trp	aat Asn	caa Gln	ctg Leu 225	gta Val	gtc Val	cct Pro	1026
gtt Val 230	ctt Leu	ttc Phe	atg Met	gtt Val	ttc Phe	tgg Trp	ctc Leu	gtc Val	tta Leu	ttt Phe	gct Ala 240	ctt Leu	cag Gln	att Ile	tac Tyr	1074
tcc Ser 245	tat Tyr	ttc Phe	agt Ser	act Thr	cga Arg	gat Asp	cag Gln	cct Pro	gca Ala	tca Ser	cgt Arg	gag Glu	agg Arg	ctt Leu 260	ctt Leu	1122
ttc Phe	ctt Leu	ttt Phe	ctg Leu	aca Thr 265	agt Ser	att Ile	gcg Ala	gaa Glu	tgc Cys	tgc Cys	agc Ser	act Thr	cct Pro	tac Tyr 275	tct Ser	1170
ctt Leu	ttg Leu	ggg Gly	ttg Leu	gtc Val	ttc Phe	acg Thr	gtt Val	tct Ser	ttt Phe	gtt Val	gcc Ala	ttg Leu	ggg Gly	gtt Val	ctc Leu	1218
aca Thr	ctc Leu	tgc Cys 295	aag Lys	ttt Phe	tac Tyr	ttg Leu	cag Gln	ggg Gly	tat Tyr	cga Arg	gct Ala	ttc Phe	atg Met	aat Asn	gat Asp	1266
cct Pro	gcc Ala	atg Met	aat Asn	cgg Arg	ggc Gly	atg Met	aca Thr	gaa Glu	gga Gly	gta Val	acg Thr	ctg Leu	tta Leu	atc Ile	ctg Leu	1314

310	315	320	
gca gtg cag act ggg ctg ata gaa ctg cag gtt gtt cat cgg gca ttc Ala Val Gln Thr Gly Leu Ile Glu Leu Gln Val Val His Arg Ala Phe 325 330 335 340			1362
ttg ctc agt att atc ctt ttc att gtc gta gct tct atc cta cag tct Leu Leu Ser Ile Ile Leu Phe Ile Val Val Ala Ser Ile Leu Gln Ser 345 350 355			1410
atg tta gaa att gca gat cct att gtt ttg gca ctg gga gca tct aga Met Leu Glu Ile Ala Asp Pro Ile Val Leu Ala Leu Gly Ala Ser Arg 360 365 370			1458
gac aag agc ttg tgg aaa cac ttc cgt gct gta agc ctt tgt tta ttt Asp Lys Ser Leu Trp Lys His Phe Arg Ala Val Ser Leu Cys Leu Phe 375 380 385			1506
tta ttg gta ttc cct gct tat atg gct tat atg att tgc cag ttt ttc Leu Leu Val Phe Pro Ala Tyr Met Ala Tyr Met Ile Cys Gln Phe Phe 390 395 400			1554
cac atg gat ttt tgg ctt ctt atc att att tcc agc agc att ctt acc His Met Asp Phe Trp Leu Leu Ile Ile Ile Ser Ser Ser Ile Leu Thr 405 410 415 420			1602
tct ctt cag gtt ctg gga aca ctt ttt att tat gtc tta ttt atg gtt Ser Leu Gln Val Leu Gly Thr Leu Phe Ile Tyr Val Leu Phe Met Val 425 430 435			1650
gag gaa ttc aga aaa gag cca gtg gaa aac atg gat gat gtc atc tac Glu Glu Phe Arg Lys Glu Pro Val Glu Asn Met Asp Asp Val Ile Tyr 440 445 450			1698
tat gtg aat ggc act tac cgc ctg ctg gag ttt ctt gtg gcc ctc tgt Tyr Val Asn Gly Thr Tyr Arg Leu Leu Glu Phe Leu Val Ala Leu Cys 455 460 465			1746
gtg gtg gcc tat ggc gtc tca gag acc atc ttt gga gaa tgg aca gtg Val Val Ala Tyr Gly Val Ser Glu Thr Ile Phe Gly Glu Trp Thr Val 470 475 480			1794
atg ggc tca atg atc atc ttc att cat tcc tac tat aac gtg tgg ctt Met Gly Ser Met Ile Ile Phe Ile His Ser Tyr Tyr Asn Val Trp Leu 485 490 495 500			1842
cgg gcc cag ctg ggg tgg aag agc ttt ctt ctc cgc agg gat gct gtg Arg Ala Gln Leu Gly Trp Lys Ser Phe Leu Leu Arg Arg Asp Ala Val 505 510 515			1890
aat aag att aaa tcg tta ccc att gct acg aaa gag cag ctt gag aaa Asn Lys Ile Lys Ser Leu Pro Ile Ala Thr Lys Glu Gln Leu Glu Lys 520 525 530			1938
cac aat gat att tgt gcc atc tgt tat cag gac atg aaa tct gct gtg			1986

ataaatttaa atttgaagat aaaaaaaaaa aaaaaaaaaa aaaaaagggc ggccgc

3630

<210> 5

<211> 663

<212> PRT

<213> Homo sapiens

<400> 5

Met	Ala	Ala	Lys	Glu	Lys	Leu	Glu	Ala	Val	Leu	Asn	Val	Ala	Leu	Arg
1				5					10					15	
Val	Pro	Ser	Ile	Met	Leu	Leu	Asp	Val	Leu	Tyr	Arg	Trp	Asp	Val	Ser
			20					25					30		
Ser	Phe	Phe	Gln	Gln	Ile	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu
		35					40					45			
Phe	Gln	Tyr	Lys	Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	Ile
	50					55				60					
Leu	Ser	Val	Val	Leu	Leu	Thr	Leu	Pro	Arg	Gln	His	Leu	Val	Gln	Leu
65					70					75					80
Tyr	Leu	Tyr	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Tyr	Ala	Gly	His	Gln	Ile
			85						90					95	
Ser	Arg	Asp	Tyr	Val	Arg	Ser	Glu	Leu	Glu	Phe	Ala	Tyr	Glu	Gly	Pro
			100					105					110		
Met	Tyr	Leu	Glu	Pro	Leu	Ser	Met	Asn	Arg	Phe	Thr	Thr	Ala	Leu	Ile
		115					120					125			
Gly	Gln	Leu	Val	Val	Cys	Thr	Leu	Cys	Ser	Cys	Val	Met	Lys	Thr	Lys
	130					135					140				
Gln	Ile	Trp	Leu	Phe	Ser	Ala	His	Met	Leu	Pro	Leu	Leu	Ala	Arg	Leu
145					150					155					160
Cys	Leu	Val	Pro	Leu	Glu	Thr	Ile	Val	Ile	Ile	Asn	Lys	Phe	Ala	Met
			165					170						175	
Ile	Phe	Thr	Gly	Leu	Glu	Val	Leu	Tyr	Phe	Leu	Gly	Ser	Asn	Leu	Leu
			180					185					190		
Val	Pro	Tyr	Asn	Leu	Ala	Lys	Ser	Ala	Tyr	Arg	Glu	Leu	Val	Gln	Val
		195					200					205			
Val	Glu	Val	Tyr	Gly	Leu	Leu	Ala	Leu	Gly	Met	Ser	Leu	Trp	Asn	Gln
	210					215					220				
Leu	Val	Val	Pro	Val	Leu	Phe	Met	Val	Phe	Trp	Leu	Val	Leu	Phe	Ala
225					230					235					240
Leu	Gln	Ile	Tyr	Ser	Tyr	Phe	Ser	Thr	Arg	Asp	Gln	Pro	Ala	Ser	Arg
			245						250					255	
Glu	Arg	Leu	Leu	Phe	Leu	Phe	Leu	Thr	Ser	Ile	Ala	Glu	Cys	Cys	Ser
			260					265					270		
Thr	Pro	Tyr	Ser	Leu	Leu	Gly	Leu	Val	Phe	Thr	Val	Ser	Phe	Val	Ala
		275					280					285			
Leu	Gly	Val	Leu	Thr	Leu	Cys	Lys	Phe	Tyr	Leu	Gln	Gly	Tyr	Arg	Ala
	290					295					300				
Phe	Met	Asn	Asp	Pro	Ala	Met	Asn	Arg	Gly	Met	Thr	Glu	Gly	Val	Thr
305					310					315					320
Leu	Leu	Ile	Leu	Ala	Val	Gln	Thr	Gly	Leu	Ile	Glu	Leu	Gln	Val	Val
			325						330					335	
His	Arg	Ala	Phe	Leu	Leu	Ser	Ile	Ile	Leu	Phe	Ile	Val	Val	Ala	Ser
			340					345					350		
Ile	Leu	Gln	Ser	Met	Leu	Glu	Ile	Ala	Asp	Pro	Ile	Val	Leu	Ala	Leu
		355				360						365			
Gly	Ala	Ser	Arg	Asp	Lys	Ser	Leu	Trp	Lys	His	Phe	Arg	Ala	Val	Ser

agc Ser	acg Thr	ggt Gly 65	tcc Ser	agg Arg	tgg Trp	agg Arg	gtc Val 70	gcc Ala	gtg Val	ccg Pro	cat His	acc Thr 75	ccg Pro	ggc Gly	ctg Leu	542
tgc Cys	acc Thr 80	agc Ser	ctg Leu	cct Pro	gac Asp	ccc Pro 85	gtc Val	aag Lys	ggc Gly	acc Thr	gag Glu 90	tgc Cys	tcc Ser	ttc Phe	tcc Ser	590
tgc Cys 95	aac Asn	gcc Ala	ggg Gly	gag Glu	ttt Phe 100	ctg Leu	gat Asp	atg Met	aag Lys	gac Asp 105	cag Gln	tca Ser	tgt Cys	aag Lys	cca Pro 110	638
tgc Cys	gct Ala	gag Glu	ggc Gly	cgc Arg 115	tac Tyr	tcc Ser	ctc Leu	ggc Gly	aca Thr 120	ggc Gly	att Ile	cgg Arg	ttt Phe 125	gat Asp	gag Glu	686
tgg Trp	gat Asp	gag Glu 130	ctg Leu	ccc Pro	cat His	ggc Gly	ttt Phe 135	gcc Ala	agc Ser	ctc Leu	tca Ser	gcc Ala 140	aac Asn	atg Met	gag Glu	734
ctg Leu	gat Asp 145	gac Asp	agt Ser	gct Ala	gct Ala	gag Glu 150	tcc Ser	acc Thr	ggg Gly	aac Asn	tgt Cys 155	act Thr	tcg Ser	tcc Ser	aag Lys	782
tgg Trp 160	gtt Val	ccc Pro	cgg Arg	ggc Gly	gac Asp 165	tac Tyr	atc Ile	gcc Ala	tcc Ser	aac Asn	acg Thr 170	gac Asp	gaa Glu	tgc Cys	aca Thr	830
gcc Ala 175	aca Thr	ctg Leu	atg Met	tac Tyr 180	gcc Ala	gtc Val	aac Asn	ctg Leu	aag Lys	caa Gln 185	tct Ser	ggc Gly	acc Thr	gtt Val	aac Asn 190	878
ttc Phe	gaa Glu	tac Tyr	tac Tyr 195	tat Tyr	cca Pro	gac Asp	tcc Ser	agc Ser 200	atc Ile	atc Ile	ttt Phe	gag Glu	ttt Phe 205	ttc Phe	gtt Val	926
cag Gln	aat Asn	gac Asp 210	cag Gln	tgc Cys	cag Gln	ccc Pro	aat Asn 215	gca Ala	gat Asp	gac Asp	tcc Ser	agg Arg 220	tgg Trp	atg Met	aag Lys	974
acc Thr	aca Thr	gag Glu 225	aaa Lys	gga Gly	tgg Trp	gaa Glu	ttc Phe 230	cac His	agt Ser	gtg Val	gag Glu 235	cta Leu 235	aat Asn	cga Arg	ggc Gly	1022
aat Asn 240	aat Asn	gtc Val	ctc Leu	tat Tyr	tgg Trp	aga Arg 245	acc Thr	aca Thr	gcc Ala	ttc Phe 250	tca Ser 250	gta Val	tgg Trp	acc Thr	aaa Lys	1070
gta Val 255	ccc Pro	aag Lys	cct Pro	gtg Val	ctg Leu 260	gtg Val	aga Arg	aac Asn	att Ile	gcc Ala 265	ata Ile	aca Thr	ggg Gly	gtg Val	gcc Ala 270	1118
tac Tyr	act Thr	tca Ser	gaa Glu 275	tgc Cys	ttc Phe	ccc Pro	tgc Cys	aaa Lys 280	cct Pro	ggc Gly	acg Thr	tat Tyr	gca Ala	gac Asp 285	aag Lys	1166

Pro Arg Gly Asp Tyr Ile Ala Ser Asn Thr Asp Glu Cys Thr Ala Thr
165 170 175
Leu Met Tyr Ala Val Asn Leu Lys Gln Ser Gly Thr Val Asn Phe Glu
180 185 190
Tyr Tyr Tyr Pro Asp Ser Ser Ile Ile Phe Glu Phe Phe Val Gln Asn
195 200 205
Asp Gln Cys Gln Pro Asn Ala Asp Asp Ser Arg Trp Met Lys Thr Thr
210 215 220
Glu Lys Gly Trp Glu Phe His Ser Val Glu Leu Asn Arg Gly Asn Asn
225 230 235 240
Val Leu Tyr Trp Arg Thr Thr Ala Phe Ser Val Trp Thr Lys Val Pro
245 250 255
Lys Pro Val Leu Val Arg Asn Ile Ala Ile Thr Gly Val Ala Tyr Thr
260 265 270
Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Tyr Ala Asp Lys Gln Gly
275 280 285
Ser Ser Phe Cys Lys Leu Cys Pro Ala Asn Ser Tyr Ser Asn Lys Gly
290 295 300
Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Gly Asp Val
305 310 315 320
Ser Glu Gly Gly Lys Ser Leu Gly Ile Glu Ser Thr Thr Lys Thr His
325 330 335
Lys Glu Ile Pro Gly Asn Arg Ala Ile Leu Leu Ala Lys Leu Arg Met
340 345 350
Val Ile Leu Lys Pro Phe Leu Ser Gly Ser Trp Asn Thr Leu Ala Asn
355 360 365
Pro Tyr Ile His
370

<210> 9
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 9
atggctgagc ctgggcacag ccaccatctc tccgccagag tcagggggaag aactgagagg 60
cgcatacccc ggctgtggcg gctgtgtctc tgggctggga ccgccttcca ggtgaccag 120
ggaacgggac cggagcttca cgcctgcaaa gagtctgagt accactatga gtacacggcg 180
tgtgacagca cgggttccag gtggaggggc gccgtgccgc ataccgccgg cctgtgcacc 240
agcctgcctg acccgtcaa gggcaccgag tgctccttct cctgcaacgc cggggagttt 300
ctggatatga aggaccagtc atgtaagcca tgcgctgagg gccgctactc cctcggcaca 360
ggcattcggg ttgatgagtg ggatgagctg ccccatggct ttgccagcct ctcagccaac 420
atggagctgg atgacagtgc tgctgagtc accgggaact gtacttcgtc caagtgggtt 480
ccccggggcg actacatcgc ctccaacacg gacgaatgca cagccacact gatgtacgcc 540
gtcaacctga agcaatctgg caccgttaac ttgcaatact actatccaga ctccagcatc 600
atctttgagt ttttcgttca gaatgaccag tgccagccca atgcagatga ctccaggtgg 660
atgaagacca cagagaaagg atgggaattc cacagtgtgg agctaaatcg aggcaataat 720
gtcctctatt ggagaaccac agccttctca gtatggacca aagtacccaa gcctgtgctg 780
gtgagaaaca ttgccataac aggggtggcc tacacttcag aatgcttccc ctgcaaacct 840
ggcacgtatg cagacaagca gggctcctct ttctgcaaac ttgcccagc caactcttat 900
tcaaataaag gagaaacttc ttgccaccag tgtgaccctg acaataactc aggtgatgtt 960
tctgaggggtg ggaagagttt ggggatagag agtaccacca aaacacacaa ggagatacca 1020
gggaatagag ccattccttct ggccaagctg aggatggtaa ttcttaaacc cttcctttct 1080
ggatcctgga atacccttgc caatccatat atccattaa 1119

Abstract The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Bursa, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the 10-year-old children in the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical activity program, while the experimental group participated in a 12-week training program. The physical fitness of the children was measured at the beginning and at the end of the 12-week period. The measurements included maximum heart rate, maximum oxygen consumption, maximum power, and maximum speed. The results of the study showed that the experimental group had significantly higher values for all four measurements at the end of the 12-week period compared to the control group. The results suggest that a 12-week training program can improve the physical fitness of 10-year-old children.

[illegible]